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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=25; hr=15; min=45; sec=10; ms=279;
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Application No: 10561041 Version No: 1.0

Input Set:**Output Set:**

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Finished: 2007-11-02 19:57:53.869
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 794 ms
Total Warnings: 42
Total Errors: 0
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

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W 402	Undefined organism found in <213> in SEQ ID (13)
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W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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W 213	Artificial or Unknown found in <213> in SEQ ID (20)
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W 213	Artificial or Unknown found in <213> in SEQ ID (22)

Input Set:

Output Set:

Started: 2007-11-02 19:57:50.075
Finished: 2007-11-02 19:57:53.869
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 794 ms
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Total Errors: 0
No. of SeqIDs Defined: 44
Actual SeqID Count: 44

Error code	Error Description
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This error has occurred more than 20 times, will not be displayed

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 TSUTSUI, HIDEKAZU
 KARASAWA, SATOSHI

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<140> 10561041

<141> 2007-11-02

<150> PCT/JP04/08786

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<170> PatentIn Ver. 3.3

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 35 40 45

Glu Lys Gly Gly Pro Leu Pro Phe Ser Val Asp Ile Leu Ser Ala Ala
 50 55 60

Phe Leu Tyr Gly Asn Arg Cys Met Thr Lys Tyr Pro Gly Gly Ile Val
 65 70 75 80
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Glu Arg Ser
 85 90 95
 Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile Arg
 100 105 110
 Leu Ser Val Glu Asp Asn Cys Phe Tyr His Glu Ser Lys Phe Ser Gly
 115 120 125
 Val Asn Phe Pro Val Asp Gly Pro Val Met Thr Leu Ala Thr Thr Gly
 130 135 140
 Trp Glu Pro Ser Ser Glu Lys Met Val Pro Ser Gly Gly Ile Val Lys
 145 150 155 160
 Gly Asp Val Thr Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg
 165 170 175
 Cys Gln Phe Asn Ser Asn Tyr Lys Ala Lys Thr Glu Pro Lys Glu Met
 180 185 190
 Pro Asp Phe His Phe Val Glu His Lys Ile Val Arg Thr Asp Leu Gly
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 His Met Glu Gly Cys Val Asn Gly His Glu Phe Thr Ile Lys Gly Glu
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 Gly Thr Gly Gln Pro Tyr Glu Gly Thr Gln Cys Ile Gln Leu Arg Val
 35 40 45

gaa aaa ggg ggt cca ttg cca ttc tca gta gac ata ttg tcg gct gcg	192
Glu Lys Gly Gly Pro Leu Pro Phe Ser Val Asp Ile Leu Ser Ala Ala	
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Phe Leu Tyr Gly Asn Arg Cys Met Thr Lys Tyr Pro Gly Gly Ile Val	
65 70 75 80	
gac tat ttc aag aac tca tgc cct gct gga tat aca tgg gaa agg tct	288
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Glu Arg Ser	
85 90 95	
ttt ctc ttt gaa gat ggc gcg gtg tgc aca gca agt gca gat ata cgc	336
Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile Arg	
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ttg agt gtc gag gat aac tgc ttt tat cac gaa tcc aag ttt agt gga	384
Leu Ser Val Glu Asp Asn Cys Phe Tyr His Glu Ser Lys Phe Ser Gly	
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gta aac ttt cct gtt gat gga cct gtg atg aca ctg gcg acg act ggt	432
Val Asn Phe Pro Val Asp Gly Pro Val Met Thr Leu Ala Thr Thr Gly	
130 135 140	
tgg gag cca tcc tcc gag aaa atg gtg ccc agt ggg ggg ata gtg aaa	480
Trp Glu Pro Ser Ser Glu Lys Met Val Pro Ser Gly Gly Ile Val Lys	
145 150 155 160	
ggg gat gtc acc atg tac ctc ctt ctg aag gat ggt ggg cgt tac cgg	528
Gly Asp Val Thr Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg	
165 170 175	
tgc cag ttc aac agt aat tac aag gca aag act gag ccg aaa gag atg	576
Cys Gln Phe Asn Ser Asn Tyr Lys Ala Lys Thr Glu Pro Lys Glu Met	
180 185 190	
cca gac ttt cac ttc gtg gag cat aag atc gta agg acc gac ctc ggt	624
Pro Asp Phe His Phe Val Glu His Lys Ile Val Arg Thr Asp Leu Gly	
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ggc cga gac cag aaa tgg caa ctg gtg gga aat tct gct gca tgt gca	672
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 Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
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 65 70 75 80
 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp
 100 105 110
 Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His
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 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu
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 165 170 175
 Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190
 Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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<222> (1)..(696)

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gta gca act ggg tac cct tac gaa ggg aaa cag atg tcc gaa tta gtg	144
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35 40 45	
atc atc aag cct gcg gga aaa ccc ctt cca ttc tcc ttt gac ata ctg	192
Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu	
50 55 60	
tca tca gtc ttt cat tat gga aac agg tgc ttc aca aag tac cct gca	240
Ser Ser Val Phe His Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala	
65 70 75 80	
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tcg tat	288
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr	
85 90 95	
gaa agg tca ttt cta ttt gaa gat gga gca gtt gct aca gcc agc tgg	336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp	
100 105 110	
aac att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc ttt cat	384
Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His	
115 120 125	
ggc gta aac ttt ccc gct gat gga ccc gta atg aaa aag cag aca att	432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile	
130 135 140	
gac tgg gag aag tcc ttc gaa aaa atg act gtg tct aaa gag gtg cta	480
Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu	
145 150 155 160	
aga ggt gat gtg act atg ttt ctt atg ctc gaa gga ggt ggt tct cac	528
Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His	
165 170 175	
aga tgc cag ttt cac tcc act tac aaa aca gag aag ccg gtc gca atg	576
Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met	
180 185 190	
ccc ccg aat cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc	624
Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly	
195 200 205	
caa agt gca aaa ggc ttt aca gtc aag ctg gaa gca cat gct gtg gct	672
Gln Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Ala His Ala Val Ala	
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His Val Asn Pro Leu Lys Val Lys	
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Val	Gly	Thr	Gly	Asn	Pro	Tyr	Glu	Gly	Lys	Gln	Met	Ser	Glu	Leu	Val
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Ile	Ile	Lys	Ser	Lys	Gly	Lys	Pro	Leu	Pro	Phe	Ser	Phe	Asp	Ile	Leu
	50					55					60				
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Asp	Met	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Asp	Gly	Met	Ser	Tyr
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Glu	Arg	Ser	Phe	Leu	Phe	Glu	Asp	Gly	Gly	Val	Ala	Thr	Ala	Ser	Trp
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Pro	Pro	Ser	His	Val	Val	Glu	His	Gln	Ile	Val	Arg	Thr	Asp	Leu	Gly
		195					200					205			
Gln	Thr	Ala	Lys	Gly	Phe	Lys	Val	Lys	Leu	Glu	Glu	His	Ala	Glu	Ala
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225					230										

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Tyr	Arg	Met	Glu	Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	
			20					25				30				

gta	gga	act	gga	aac	cct	tac	gaa	ggg	aaa	cag	atg	tcc	gaa	tta	gtg	144
Val	Gly	Thr	Gly	Asn	Pro	Tyr	Glu	Gly	Lys	Gln	Met	Ser	Glu	Leu	Val	
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atc	atc	aag	tct	aag	gga	aaa	ccc	ctt	cca	ttc	tcc	ttt	gac	ata	ctg	192
Ile	Ile	Lys	Ser	Lys	Gly	Lys	Pro	Leu	Pro	Phe	Ser	Phe	Asp	Ile	Leu	
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tca	aca	gcc	ttt	caa	tat	gga	aac	aga	tgc	ttc	aca	aag	tac	cct	gca	240
Ser	Thr	Ala	Phe	Gln	Tyr	Gly	Asn	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Ala	
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gac	atg	cct	gac	tat	ttc	aag	caa	gca	ttc	cca	gat	gga	atg	tca	tat	288
Asp	Met	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Asp	Gly	Met	Ser	Tyr	
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gaa	agg	tca	ttt	cta	ttt	gag	gat	gga	gga	gtt	gct	aca	gcc	agc	tgg	336
Glu	Arg	Ser	Phe	Leu	Phe	Glu	Asp	Gly	Gly	Val	Ala	Thr	Ala	Ser	Trp	
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agc	att	cgt	ctc	gaa	gga	aat	tgc	ttc	atc	cac	aat	tcc	atc	tat	cat	384
Ser	Ile	Arg	Leu	Glu	Gly	Asn	Cys	Phe	Ile	His	Asn	Ser	Ile	Tyr	His	
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Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Gln	Thr	Ile	
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ggc	tgg	gat	aag	tcc	ttc	gaa	aaa	atg	agt	gtg	gct	aaa	gag	gtg	cta	480
Gly	Trp	Asp	Lys	Ser	Phe	Glu	Lys	Met	Ser	Val	Ala	Lys	Glu	Val	Leu	
145					150					155				160		

aga	ggc	gat	gtg	act	cag	ttt	ctt	ctg	ctc	gaa	gga	ggc	ggc	tac	cag	528
Arg	Gly	Asp	Val	Thr	Gln	Phe	Leu	Leu	Leu	Glu	Gly	Gly	Gly	Tyr	Gln	
				165					170					175		

aga	tgc	cgg	ttt	cac	tcc	act	tac	aaa	acg	gag	aag	cca	gtc	gca	atg	576
Arg	Cys	Arg	Phe	His	Ser	Thr	Tyr	Lys	Thr	Glu	Lys	Pro	Val	Ala	Met	
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ccc	ccg	agt	cat	gtc	gta	gaa	cat	caa	att	gtg	agg	acc	gac	ctt	ggc	624
Pro	Pro	Ser	His	Val	Val	Glu	His	Gln	Ile	Val	Arg	Thr	Asp	Leu	Gly	
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 35 40 45

Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60

Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
 65 70 75 80

Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95

Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
 100 105 110

Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
 115 120 125

Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140

Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
 145 150 155 160

Arg Gly Asp Val Thr His Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
 165 170 175

Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190

Pro Pro Ser His Val Val Glu His